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# Analysis of evolutionary process in a lot sizing application

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**Abstract**

This paper seeks to determine the relationship between the best chromosome and its ancestors in genetic algorithms. The domain chosen is that of the classical lot sizing problem. A genetic algorithm software is developed to find the best lot size. We trace the best chromosome back for all generations to its ancestors and observe the evolutionary process. The preliminary results show that not all promising solutions led to the best chromosome. There were several good chromosomes repeating from generation to generation in the later part of the process and eventually leading to the best chromosome.

Keywords: analysis of evolutionary process, ancestors, lot sizing application

## 1. Introduction

The main purpose of this paper is to perform a preliminary investigation into the evolutionary process of genetic algorithms. An attempt is made to find out how good solutions evolve from the initial population and which chromosomes in each generation eventually contribute to the best solution. Furthermore, the percentage of similarity is also identified for these important chromosomes during the evolutionary process.

The application domain is the lot sizing area. Lot sizing is one of the key elements in production management. Lot sizing determines the quantity and timing of orders. These orders are determined at the beginning of planning period and released in the identified periods. In this study, shortages are not allowed. The lot size identified for one period depends not only on the demand for that period, but also depends on the demand for the following periods. There are various methods for computing lot sizes including genetic algorithms. The objective is to minimize the total cost of inventory carrying and setup costs.

## 2. Literature Review

The literature given in this paragraph briefly discusses GA applications in lot sizing. Hernandez and Süer (1999) developed a genetic algorithm application for single-item lot sizing problem. They also studied the impact of scaling on the performance of the GA. Hop et al. (2005) proposed an adaptive genetic algorithm for this problem. The adaptive GA provided bad solutions in the initial generations, but then improved quickly and finally found better solutions when compared with Silver-Meal procedure. Gaafar et al. (2006) also proposed a GA approach where

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orders have to be integer multiples of a fixed quantity. They proposed multiple crossover and mutation operators. The results indicate that the GA performed better than the modified Silver-Meal (SM) approach on 16 cases. Süer, Badurdeen and Dissanayake (2008) proposed a multi-chromosome crossover strategy for a capacitated multi-item lot sizing problem. They also included labor cost in their study. Chromosome segments were grouped into three categories and more than two chromosomes could be involved in the generation of an offspring. The results outperformed classical GA approach.

## 3. Methodology

In this paper, a binary representation is used for chromosome definition. The chromosome consists of *t* genes where *t* is the number of periods in the planning horizon. In this binary representation "1" in a period means that an order will be placed in that period. The order size includes all the requirements in this particular period and all consecutive "0" periods (until another period with "1" is reached again). The first gene always takes a value of 1 to avoid shortages. This concept can be illustrated with an example given in Figure 1 where there are six periods in the planning horizon. The first order is placed in period 1 and covers requirements for the first three periods, the second order is placed in period 4 and the third order is placed in period 5 and covers requirements of periods 5 and 6.

Table 1: Chromosome representation for a lot sizing problem

| Period | 1 | 2 | 3 | 4 | 5 | 6 |
|---|---|---|---|---|---|---|
| Chromosome | 1 | 0 | 0 | 1 | 1 | 0 |
| Net Requirements | 50 | 40 | 50 | 30 | 60 | 20 |
| Order Size | 140 | | | 30 | 80 | |

The data used in the experimentation is given in Table 2. The inventory carrying cost is $1/unit/period and ordering cost is $100/order. A genetic algorithm software is developed and used to track the ancestors of the best chromosome. The software records the chromosome structures, their similarity to the best chromosome, cut points, fitness functions, parents of each chromosome and all other related information about all chromosomes for all generations. It writes this data to a text file. The fitness function is the total cost fo setup and inventory carrying costs.

Table 2: Net requirements for all periods

| Periods | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
|---|---|---|---|---|---|---|---|---|---|---|
| Requirements | 50 | 70 | 60 | 110 | 20 | 40 | 80 | 60 | 50 | 40 |

The settings used in the experimentation for period size, population size, crossover and mutation probability, and the selection mode of population are shown in Table 3.

Table 3: Settings used in the experimentations

| Setting | Length of planning horizon | Population size | Crossover probability | Mutation probability | Selection mode |
|---|---|---|---|---|---|
| Parameter | 10 | 10 | 0.7 | 0.1 | Random |

## 4. Analysis and Results

In this experimentation, the number of generations is set to 500. Figure 1 shows the chromosomes in the initial population and their fitness function values and similarity to the best chromosome and other relevant information. Similarity is found by dividing the number of shared genes with the best chromosome to the number of periods by ignoring the first gene. Since the first gene has to be 1 at all chromosomes, it is not included while finding similarity values. This is a good measure of commonality and thus the similarity level between two chromosomes. For example, chromosome 4 has five common genes out of nine with the best chromosome with a similarity of 0.55.

GA found the best result first at the 15th generation with a fitness function value of 760. Figure 2 illustrates the fitness function values through all generations. It is evident that the software found the best fitness function in several generations. Only the ancestors of the first best result is analysed in this paper.

Table 4 shows some of the ancestors of the best chromosome all the way back to the initial population. Chromosome type represents ID numbers for repeating chromosomes during the entire evolutionary process. For non-repeating chromosomes, no number but capital letter U (unique) is assigned. It can be seen that many chromosomes repeat at various generations. Indeed, the same chromosome type exists in one generation with more than one copy as seen in generation 13.

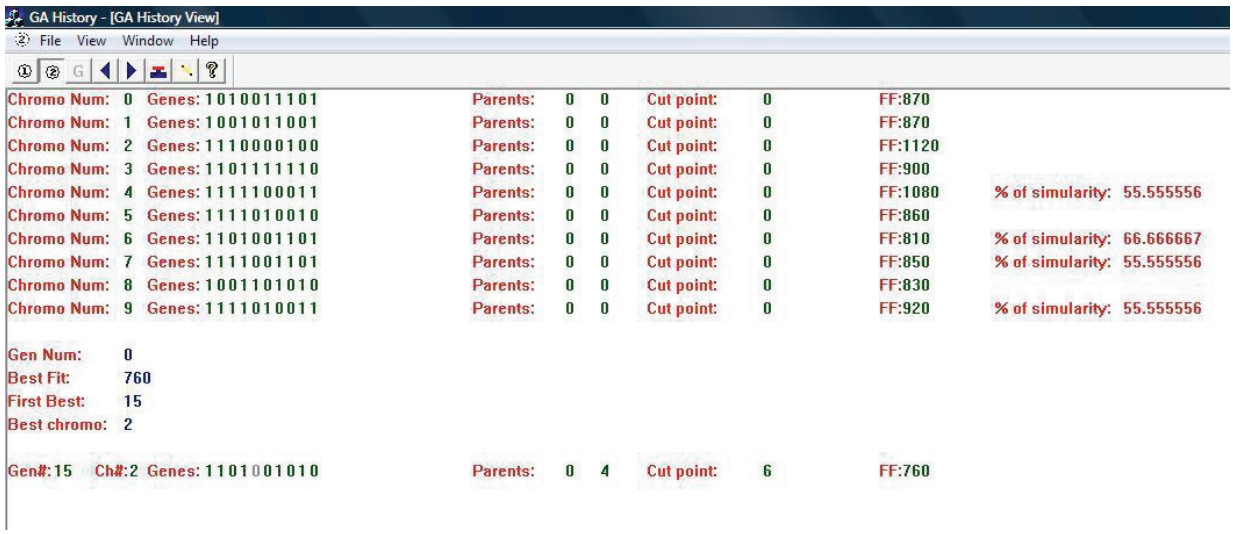


Figure 1. Results and initial population data for the experimentation

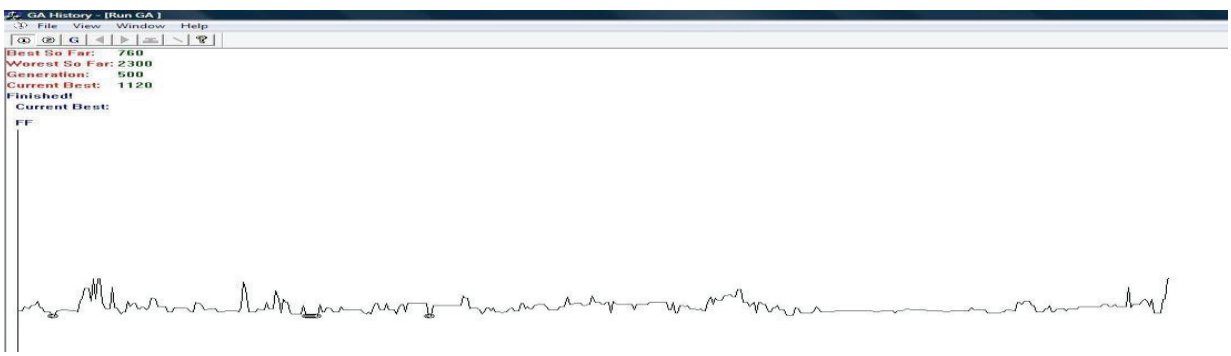


Figure 2. Graphical representation of fitness functions by generations

Table 4: History of the best chromosome

| Gen. # | Chr. # | Chromosome | Chromosome type | Parents | | cut point | FF | Similarity to the best chromosome | Ave. sim. | Min. sim. | Max. sim |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 15 | 2 | 1101001010 | Best | 0 | 4 | 6 | 760 | | | | |
| 14 | 0 | 1111101010 | 11 | 2 | 7 | 5 | 840 | 77.8 | 83.3 | 77.8 | 88.9 |
| | 4 | 1101101010 | 12 | 5 | 5 | 6 | 800 | 88.9 | | | |
| 13 | 2 | 1111101010 | 11 | 5 | 5 | 2 | 840 | 77.8 | 81.5 | 77.8 | 88.9 |
| | 5 | 1101101010 | 12 | 6 | 6 | 6 | 800 | 88.9 | | | |
| | 7 | 1111101010 | 11 | 6 | 8 | 7 | 840 | 77.8 | | | |
| …. | | | | | | | | | | | |
| 0 | 4 | 1111100011 | 3 | | | | 1080 | 55.6 | 58.3 | 55.6 | 66.7 |
| | 6 | 1101001101 | 2 | | | | 810 | 66.7 | | | |
| | 7 | 1111001101 | U | | | | 850 | 55.6 | | | |
| | 9 | 1111010011 | 1 | | | | 920 | 55.6 | | | |

In the initial population, generation 0, chromosomes 4 and 7 have the same similarity even though they have significantly different fitness function values, 1080 and 850, respectively. In early generations, minimum, average and maximum similarities did not show a very clear pattern. However, as we got closer to the best chromosome, all three measures increased. Figure 3 shows the change in similarity values by generations.

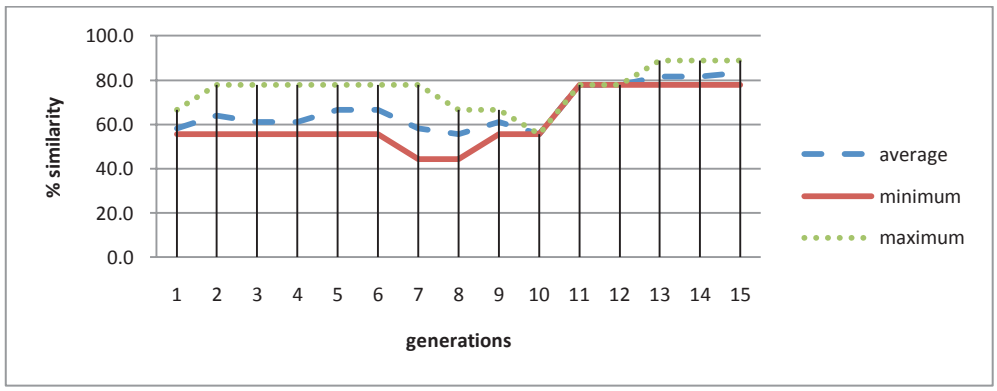


Figure 3. Change in similarities by generations

In Table 5, various chromosomes are listed in the order of increasing fitness function values along with generations they were observed and average similarity values.

Table 5: Chromosome types and generation numbers

| Chromosome Type | Chromosome | Generation numbers | Fitness Function | Average Similarity |
|---|---|---|---|---|
| 12 | 1101101010 | 14,13,12 | 800 | 88.9 |
| 2 | 1101001101 | 1,0 | 810 | 66.7 |
| 9 | 1111001100 | 5 | 830 | 66.7 |
| 11 | 1111101010 | 14,13,12,11,10 | 840 | 77.8 |
| 5 | 1101101101 | 3,2 | 850 | 55.6 |
| 8 | 1111001001 | 7,6,5,4 | 860 | 66.7 |
| 4 | 1111001011 | 6,5,4,3,2,1 | 860 | 77.8 |
| 7 | 1110001100 | 5,4,3,2 | 900 | 55.6 |
| 6 | 1111101001 | 9,8,3,2 | 900 | 55.6 |
| 10 | 1110101001 | 7,6 | 910 | 44.4 |
| 1 | 1111010011 | 1,0 | 920 | 55.6 |
| 3 | 1111100011 | 1,0 | 1080 | 55.6 |
| 13 | 1110000110 | 9 | 1130 | 55.6 |
| 14 | 1100001111 | 8 | 1100 | 66.7 |
| U | N/A | 15,7,0 | N/A | N/A |

The following conclusions can be drawn from Table 4 and Table 5:

1. There are only 3 unique and 14 repeating chromosomes in the 15-generation-family-tree. There are $2^9$ (=512) different possible chromosome types.
2. Good chromosomes which have better fitness function values tend to repeat more than bad chromosomes. (i.e. chromosomes 11, 12, 8, and 4)

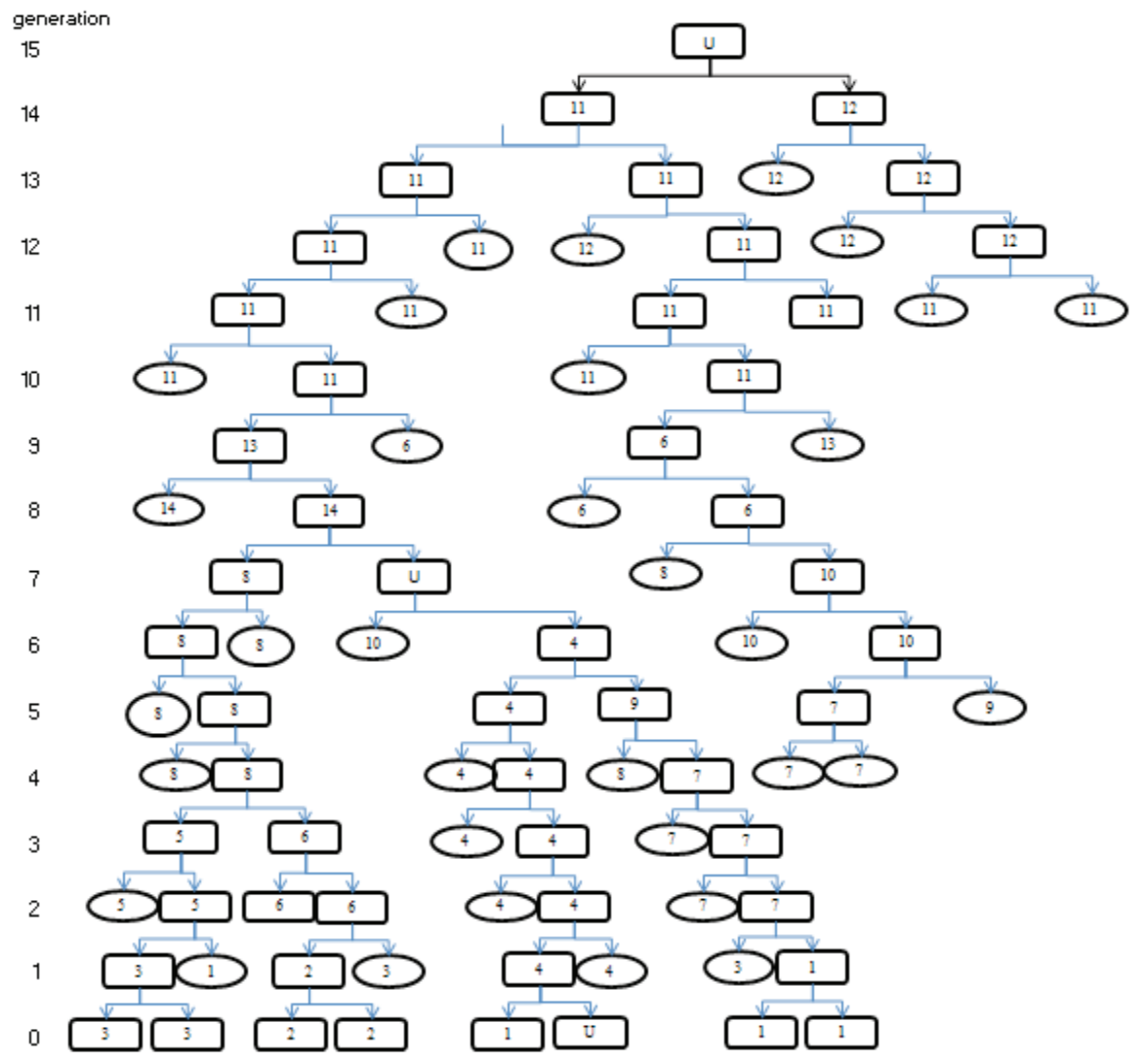


Figure 4. Family tree of the best chromosome

3. Good chromosomes tend to repeat more at closer generations to the best chromosome generation (i.e., chromosomes 11 and 12)
4. Increased similarity to the best chromosome does not necessarily mean better fitness function value. For example chromosome type 14 and chromosome type 8 has same similarity, but they have 1100 and 860 as fitness functions, respectively. Similarly, chromosome 5 has lower similarity than these two chromosomes but better fitness function value.
5. Bad chromosomes repeat at only beginning generations. (i.e. chromosomes 1 and 3)
6. Chromosome 11 is the most repeating chromosome, it repeats almost twice at every generation it exists.

Table 6: Gene representation of the best chromosome and chromosomes 11 and 12

| Chr | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | FF | similarity |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Best | **1** | **1** | **0** | **1** | 0 | **0** | **1** | **0** | **1** | **0** | 760 | 100 |
| 12 | **1** | **1** | **0** | **1** | 1 | **0** | **1** | **0** | **1** | **0** | 800 | 88.9 |
| 11 | **1** | **1** | 1 | **1** | 1 | **0** | **1** | **0** | **1** | **0** | 840 | 77.8 |

7. There are only 2 different chromosomes, namely chromosomes 11 and 12, at generations 10, 11, 12, 13 and 14. This means that only these two chromosomes went through mating process with each other.

Table 6 is formed to compare the genes of the best chromosome and the most repeating chromosomes, 11 and 12, at closer generations to generation 15. This table shows that 8 genes are repeating, namely genes 1, 2, 4, 6, 7, 8, 9 and 10 at all of these chromosomes. Among these, the last five genes and the first 2 genes form blocks.

A family tree is formed in order to have a graphical illustration of the ancestors of the best chromosome. Figure 4 shows the family tree of the best chromosome. It starts from the 15$^{th}$ generation and goes back to the initial population. In the figure, the circles represent the fathomed offsprings, meaning there is more than one copy of chromosome from that chromosome type at that generation level and tracing only one of them is enough to find the previous ancestors. Rectangles are the offsprings to be traced to the initial population. Repeating chromosomes at each generation can be seen easily in the same figure. Chromosomes 11 and 12 dominate the following generations starting from generation 10. Figure 4 can be used to identify initial population chromosomes that represent the best chromosome. Chromosomes 6, 7, 9 and 4 are ancestors (contributors) of the best chromosome. Table 7 shows properties of these chromosomes as well as non-contributing chromosomes. It is surprising to see that some of the better chromosomes (with respect to both fitness and similarity coefficients) were not involved in evolutionary processes in finding the best chromosome.

Table 7: Fitness functions and similarities of ancestors' of the best chromosome at initial population

| Non-contributors | | | Contributors | | |
|---|---|---|---|---|---|
| Chromosome number | FF | sim. | Chromosome number | FF | sim. |
| 8 | 830 | 0.778 | 6 | 810 | 66.5 |
| 5 | 860 | 0.667 | 7 | 850 | 55.6 |
| 0 | 870 | 0.222 | 9 | 920 | 55.6 |
| 1 | 870 | 0.556 | 4 | 1080 | 55.6 |
| 3 | 900 | 0.667 | | | |
| 2 | 1120 | 0.444 | | | |

## 5. Conclusions

The GA History software gives us useful inside information about the history of the best chromosome. It may be used to determine good gene blocks and good chromosomes for the initial population. The preliminary results show that better chromosomes in the initial population may not contribute to the best chromosome at the end. There are also surprising results in terms of similarity and the fitness function value, i.e., there may be good chromosomes with high fitness values but very low similarity to the best chromosome. As to the evolutionary process, there were several good chromosomes repeating from generation to generation in the later part of the process that eventually led to the best chromosome. Some good chromosomes dropped out as the number of generations increased even though they were promising at the beginning. We believe that there is more work that needs to be done to study the evolutionary process and discover relations (if any) with different problems and in different domains.

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